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Tools for text mining over biomedical literature

Rinaldi, Fabio ; Schneider, G ; Kaljurand, K ; Hess, M

Abstract: This poster describes OntoGene: an environment, based on a deep linguistic parser, aimed at supporting the process of Text Mining from Biomedical Scientific Literature. We will illustrate in particular the Relation Extraction component and the development support facilities.

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An Environment for Relation Mining over Richly Annotated Corpora: the case of GENIA

Fabio Rinaldi*, Gerold Schneider*, Kaarel Kaljurand*, Michael Hess*, Martin Romacker**

Abstract

The biomedical domain is witnessing a rapid growth of the amount of published scientific results, which makes it increasingly difficult to filter the core information. There is a real need for support tools that ‘digest’ the published results and extract the most important information.

We describe and evaluate an environment supporting the extraction of domain-specific relations, such as protein-protein interactions, from a richly-annotated corpus. We use full, deep-linguistic parsing and manually created, versatile patterns, expressing a large set of syntactic alternations, plus semantic ontology information.

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